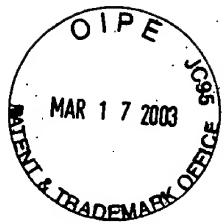


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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

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- (F) POSTAL CODE (ZIP): G11 7HX

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 - (B) STREET: 4 Upway Road
 - (C) CITY: Oxford
 - (E) COUNTRY: United Kingdom
 - (F) POSTAL CODE (ZIP): OX3 9QH

(ii) TITLE OF INVENTION: AVIAN GHD GENES AND THEIR USE IN METHODS FOR
SEX IDENTIFICATION IN BIRDS

(iii) NUMBER OF SEQUENCES: 39

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: WO PCT/GB96/01341

(B) FILING DATE: 05-JUN-1996

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: GB 9511439.3

(B) FILING DATE: 06-JUN-1995

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Warren M Cheek, Jr.

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(C) REFERENCE/DOCKET NUMBER: 263/PPNTIR1172US

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(A) TELEPHONE: (202)-721-8200

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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 723 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CCCGGTCAAGG AATGACTAGA TGTGGCACTT AGTGCATGG TCTAGTTGAC	60
AAGGTGATGG TTGGTCAAAA GTTGGACTCG ATGATCTCAG AGTTTTTTC CAGCCTTAAT	120
AATTCTATGA ATTCTGTAAT TTTATTCTTG ATCTTTTGA GCGAAGTTG TTTGGGGATT	180
TTAGTTGGT TTCCCTGTCA CTGTTTCTT TCCTTGAAAC TGACTTCAT TTGCAACATG	240
AGAATTGCTG TATTTGTCAG GTTACAAGTA GTGCAATGGC TGCTTAGAAG TAGTGAGAAA	300
CATTTAGGGA AATACTGGAG TGAAGCAAAC ACAGTGGTAC TGCCAAACTG TAGCTTGAGG	360
ATTTGAGGAG CCACAGAGTT GTATATAAAT TTGTTTAATG ATATCCTGCC CCTGCCTTCC	420
ATTAATTGCT TGTTTATGA AACCACTCTT TTTTTTTTT TTTTTTTTT GGCTTCTTCA	480
TATCCTGTGG TAATGAGTTA ATGCATTTAG AAGCACATGG CAGAACTAGG AGATCTGTGG	540
ATGACAGTGG TACAGGAGCT CTGAATTTT TAGATAAACT ATGAGAGTGG AAACAGAAAT	600
CTGAGGCTAG TTTCTTGAGC TGACTGTAAA TTTTGTGAGA ATATTTCAA GACTACATTA	660
GTTGTGTGTT TGAGGAAAAA TAAAATGTTT AAGTTGTCCA TTCCTTGAAA CCTCCCCGACC	720
GGG	723

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATTCTTCCAG ATGATCCTGA TAAAAAACCA CAAGCAAAAC AGTTACAGAC CAAAAAACCA	60
CAAGCAAAAC AGTTACAGAC CCGTGCAGAC TACCTCATCA AACTACTTAG CAGAGATCTT	120
GCAAAAAGAG AGGCTCAGAG ACTTTGTGGT GCG	153

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATTTTACCTG ATGATCCAGA CAAGAAACCC CAGGCAAAGC AGCTACAGAC CAAGAAACCC	60
CAGGCAAAGC AGCTACAGAC CCGTGCAGAC TACCTCATTA AATTACTGAA TAAAGACCTT	120
GCAAGAAAGG AAGCACAAAG GCTTGCTGGT GCA	153

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATTTTACCTG ATGATCCAGA TAAGAAACCC CAGGCTAACGC AGTTACAGAC CAAGAAACCC	60
CAGGCTAACGC AGTTACAGAC CCGTGCAGAT TACCTCATTA AATTACTGAA TAAAGACCTT	120
GCAAGAAAGG AAGCACAGAG ACTTGCTGGT GCA	153

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATTTTACCTG ATGACCCAGA TAAGAAACCA CAGGCAAAGC AGTTGCAGAC CAAGAAACCA	60
CAGGCAAAGC AGTTGCAGAC CCGTGCAGAT TACCTCATTA AATTACTGAA TAAAGACCTT	120
GCAAGAAAAG AAGTGCAAAG ACTTACTGGT GCA	153

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln

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1	5	10	15
Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Ser Arg Asp Leu Ala Lys			
20	25	30	
Arg Glu Ala Gln Arg Leu Cys Gly Ala			
35	40		

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Ile	Leu	Pro	Asp	Asp	Pro	Asp	Lys	Lys	Pro	Gln	Ala	Lys	Gln	Leu	Gln
1	5	10	15												
Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg															
20	25	30													
Lys Glu Ala Gln Arg Leu Ala Gly Ala															
35	40														

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln

1

5

10

15

Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg

20

25

30

Lys Glu Ala Gln Arg Leu Ala Gly Ala

35

40

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln

1

5

10

15

Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg

20

25

30

Lys Glu Val Gln Arg Leu Thr Gly Ala

35

40

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CGGGCTGCGG CACGAAGCGC ACCGCCGGCG CACGCAGGCT CGGGCCGGGG AAGGCCTGGC	60
CCGCCGAGCC GGACGCACGC AGGTATTTGG GCAAAAATCT TGGCCATCTG TAGAGAATAG	120
CAAGTCAAAC GCATTACTTC GAAACATAC GGAGTACCAAG AAAGGGGATT CTTGACCTAC	180
ACCTTGTAAC CTGAGTGGAC TTTCTTTTA ACTTCTTAAT ACTTACAATG AATGGGCACA	240
GTGATGAAGA AAGTGTAAAGA AACAGCAGTG GAGAGTCAAG CAGATCAGAT GATGATTCTG	300
GGTCAGCTTC AGGTTCTGGA TCTGGTTCAA GCTCTGGAAG CAGTAGCGAT GGAAGTAGCA	360
GCCAGTCAGG TAGCAGTGAC TCTGAATCTG GTTCAGAGTC AGGCAGTCAA TCCGAATCAG	420
AGTCTGACAC ATCTAGAGAG AAGAAACAAG TTCAAGCTAA ACCTCCGAAA GCTGACGGAT	480
CTGAGTTTG GAAGTCCAGT CCAAGCATAAC TTGCTGTACA GAGATCAGCA GTGCTCAAGA	540
AGCAACAGCA ACAGCAAAAAA GCAGCATCAT CAGACAGTGG TTCAGAAGAG GACTCATCCA	600
GTAGTGAAGA TTCTGCCGAT GATTGTCCA GTGAAACTAA GAAGAAAAAG CATAAAGATG	660
AAGACTGGCA AATGTCAGGG TCAGGGTCAG TATCAGGAAC TGTTCTGAT TCTGAATCGG	720
CGGAAGATGG GGATAAAAGC AGTTGTGAAG AAAGTGAATC TGACTATGAG CCAAAAAACA	780
AAGTCAAAAG CCGTAAACCT CCAAGCAGAA TTAAGCCAAA AAGTGGAAA AAGAGCACAG	840
GACAGAAGAA GAGGCAACTT GATTGTACAG AGGAGGAGGA GGACGATGAT GAAGATTATG	900
ATAAGAGAGG ATCTCGTCGC CAGGCAACAG TGAATGTTAG TTACAAAGAA GCTGAAGAAA	960
CCAAGACAGA TTCTGATGAT TTGCTGGAAG TTTGTGGAGA GGATGTCCCCA CAGACTGAAG	1020

AAGATGAATT TGAAACTATA GAGAAGTTA TGGACAGTCG AATTGGCCGA AAAGGAGCCA	1080
CTGGTGCCTC AACCACCATC TATGCCGTTG AGGCAGATGG TGACCCAAAT GCTGGGTTG	1140
AAAAGTCAAA GGAGCTGGGA GAAATACAGT ATCTTATTAA ATGGAAAGGC TGGTCACACA	1200
TCCATAACAC TTGGGAAACT GAAGAACGC TGAAGCAACA AAATGTTAAA GGAATGAACA	1260
AACTGGACAA CTACAAGAAA AAGGATCAGG AGACAAAACG CTGGCTGAAA AATGCTTCTC	1320
CAGAAGATGT GGAATATTAT AACTGCCAGC AGGAGCTTAC AGATGATCTG CACAAACAAT	1380
ATCAAATAGT GGAAAGAATA ATTGCTCATT CAAATCAAAA GTCAGCAGCT GTTATCCGG	1440
ACTACTATTG CAAATGGCAG GGTCTGCCTT ACTCAGAATG TAGCTGGAA GATGGTGCTC	1500
TCATTGCCAA AAAGTTTCAG GCACGCATTG ATGAGTATT TAGCAGAAAT CAATCCAAGA	1560
CTACTCCCTT TAAGGACTGC AAGGTTCTAA AACAGAGACC AAGATTGTT GCACTGAAGA	1620
AGCAACCATC TTACATTGGA GGACATGAAA GTCTGGAGTT AAGAGATTAT CAGTTAAATG	1680
GATTGAATTG GCTCGCTCAT TCATGGTGCA AAGGAAATAG TTGTATTCTT GCAGATGAAA	1740
TGGGTCTGGG TAAAACAATA CAAACAATT CTCTCTGAA CTACCTGTT CATGAACATC	1800
AACTGTATGG CCCTTTCTT CTGCGCGTGC CACTTCTAC CTTGACATCT TGGCAAAGAG	1860
AGATTCAAAC TTGGGCTCCT CAGATGAATG CTGTAGTTA CTTAGGAGAT ATAACTAGTA	1920
GAAATATGAT AAGGACTCAT GAATGGATGC ATCCACAGAC TAAACGATTA AAGTTAACCA	1980
TACTTCTGAC GACATATGAA ATTTACTGA AGGATAAGTC ATTCCTGGT GGTCTCAATT	2040
GGGCATTCAT AGGAGTTGAT GAAGCTCATC GTTTAAAAAA TGATGACTCT CTTCTGTACA	2100
GGACTTTAAT AGACTTTAAG TCCAACCATC GACTTCTGAT TACTGGAACC CCAC TGCAAA	2160
ATTCCCTCAA AGAGCTGTGG TCTTGTGC ATTCATCAT GCCAGAAAAA TTTCCCTCCT	2220
GGGAAGATTT TGAAGAGGAG CATGGCAAAG GAAGAGAGTA TGGTTATGCA AGTCTTCACA	2280
AAGAGCTTGA ACCATTTTA CTAAGAAGAG TTAAAAAAGA TGTAGAAAAG TCTTACCTG	2340
CTAAGGTTGA ACAAAATTCTG AGGATGGAAA TGAGTGCATT GCAGAAGCAA TATTACAAGT	2400
GGATTTAAC AAGGAATTAT AAAGCCCTCA GTAAAGGTTA AAAAGGCAGT ACCTCAGGCT	2460
TTCTGAACAT TATGATGGAA CTTAAGAAGT GTTGTAAACCA TTGCTACCTC ATTAAGGCCAC	2520

CAGATGATAA TGAATTCTAT AATAAACAGG AGGCCTTACA GCATTTGATA CGTAGCAGCG	2580
GGAAACTAAT CCTTCTTGAC AAGCTACTGA TTCGTCTGCG AGAACGTGGC AACAGAGTTC	2640
TGATTTCTC TCAGATGGTG AGGATGCTGG ACATCCTAGC AGAATATCTG AAGTATCGCC	2700
AGTTTCCCTT CCAGAGACTT GATGGATCAA TAAAAGGGGA ATTGAGGAAG CAAGCACTGG	2760
ATCATTCAA TGCAGAAGGA TCAGAGGATT TCTGTTTTT ACTGTCTACA AGAGCTGGAG	2820
GATTAGGTAT TAACTTGGCA TCTGCTGACA CTGTAGTTAT TTTGATTCT GACTGGAATC	2880
CACAGAATGA TCTGCAGGCA CAGGCCAGAG CTCATAGAAT TGGACAGAAG AAACAGGTTA	2940
ATATTATCG GCTAGTCACA AAAGGATCAG TAGAAGAAGA TATTCTTGAA AGAGCCAAGA	3000
AGAAGATGGT GCTAGACCAC TTAGTAATTAGAAGA CACGACAGGA AAAACTGTTCA	3060
TGCATACAGG TTCAACTCCA TCAAGCTCTA CACCTTTAA TAAAGAAGAG TTATCAGCTA	3120
TTTGAAAGTT TGGTGCTGAG GAACTCTTAA AAGAACCTGA AGGAGAAGAA CAGGAGCCCC	3180
AGGAAATGGA TATAGATGAA ATCTTGAAGA GAGCTGAAAC TCGGGAAAAT GAGCCAGGTC	3240
CATTGACTGT AGGGGATGAG TTGCTTCAC AGTTCAAGGT GGCGAACTTT TCCAATATGG	3300
ATGAAGATGA TATTGAGTTG GAACCAGAAA GAAATTCAAG AAATTGGGAA GAAATCATCC	3360
CAGAATCCC ACGGAGAAGG ATAGAGGAGG AGGAAAGACA AAAAGAACTT GAAGAAATAT	3420
ACATGCTCCC GAGGATGAGA AACTGTGCAA AACAGATCAG CTTTAATGGG AGTGAAGGAA	3480
GACGCAGTAG GAGCAGAAGA TATTCTGGAT CTGATAGTGA CTCCATCACA GAAAGAAAAC	3540
GGCCAAAAAA GCGTGGAAAGA CCTCGAACCA TTCCTCGAGA AAATATTAAA GGATTTAGTG	3600
ATGCAGAGAT CAGGCGGTTT ATCAAGAGTT ACAAGAAATT TGGTGGCCCT CTGGAAAGGT	3660
TAGATGCTGT AGCTAGAGAT GCTGAACCTGG TTGATAAATC TGAGACAGAC CTTAGACGTT	3720
TGGGTGAACT TGTACATAAT GGATGCATTA AGGCTTTAAA GGACAATTCA TCTGGACAAG	3780
AAAGAGCAGG AGGTAGACTT GGGAAAGTTA AAGGCCAAC GTTTCGAATC TCAGGAGTGC	3840
AGGTGAATGC AAAACTAGTC ATCTCTCACG AAGAAGAGCT GGCACCACTG CACAAATCCA	3900
TTCCTTCAGA TCCAGAAGAA AGGAAAAGAT ATGTCATCCC ATGCCACACC AAGGCTGCTC	3960
ACTTCGATAT AGATTGGGGT AAAGAAGATG ATTCCAATCT GTTAGTAGGC ATCTATGAAT	4020

ATGGCTATGG CAGCTGGAA ATGATAAAAA TGGATCCAGA TCTCAGCTTA ACACAGAAGA	4080
TTTTACCTGA TGATCCAGAC AAGAAACCCC AGGCAAAGCA GCTACAGACC CGTGCAGACT	4140
ACCTCATTAA ATTACTGAAT AAAGACCTTG CAAGAAAGGA AGCACAAAGG CTTGCTGGTG	4200
CAGGCAATTG CAAGAGAAGG AAGACAAGAA ATAAGAAGAA TAAGATGAAG GCTTCAAAAA	4260
TAAAAGAAGA AATAAAGAGT GATTCTCAC CACAACCCTC AGAAAAATCT GATGAAGATG	4320
ATGAGGAGGA GGATAACAAG GTAAATGAAA TGAAATCTGA AAATAAAGAA AAATCTAAA	4380
AAATTCCATT GCTGGATACT CCAGTTCAT A TTACTGCAAC CAGTGAACCA GTTCCTATCT	4440
CAGAAGAACATC TGAAGAACTC CATCAGAAGA CATTAGTGT GTGCAAAGAA AGAATGAGGC	4500
CTGTCAAAGC AGCACTGAAA CAGCTGGATA GACCAGAGAA GGGCCTTCT GAAAGGGAGC	4560
AGCTGGAACA TACTAGGCAG TGTCTAATCA AAATTGGGA TCACATTACA GAATGCCTGA	4620
AGGAGTACAC AAATCCGAG CAAATAAAC AGTGGAGGAA AAATTGTGG ATTTTGTGT	4680
CCAAGTTAC AGAATTGAT GCCAGAAAGC TGCACAAACT CTACAAACAT GCAATCAAA	4740
AGCGCCAAGA GTCTCAGCAA CACAATGACC AAAACATTAG CAGCAATGTG AATACACATG	4800
TAATCAGAAA TCCAGATGTG GAAAGACTGA AGGAGACTAC AAACCATGAT GATAGTAGCA	4860
GGGACAGTTA TTCTTCTGAT AGACATTTAT CACAATACCA TGATCATCAC AAAGACAGGC	4920
ATCAGGGAGA TGCTTACAAG AAAAGTGA CTTCCAGACT CCAGGAAAG GCCATATTCA GCCTTCAGTA	4980
ATGGAAAAGA TCACAGAGAC TGGGATCACT ACAAAACAGGA CAGCAGATAC TACAGTGATA	5040
GTAAACATAG AAAGTTAGAT GACCACAGGA GCAGAGACCA CAGGTCAAAC CTGGAAGGAA	5100
ACTTAAAAGA CAGCCGGGT CATTAGATC ACCGCTCCC TTCAGACCC ACCAGACACT	5160
CAGATCACCG TTCCACTTCA GAATACAGCC ATCATAAACAT TTGAGAGAT TATAGATACC	5220
ACTCAGACTG GCAAATGGAC CACAGAGCTT CTGGTAGTGG CCCGAGGTCA CCACTAGATC	5280
AGAGGTCTCC TTATGGTTCA AGATCTCCCC TAGGACACAG ATCTCCATT GAAACACTCAT	5340
CAGATCACAA AAGTACACCT GAACATACAT GGAGTAGCCG GAAGACATAA CAAAGACTGA	5400
CATTTCTGG ACCTTCTTT TAGCCATATA CAGTAAACTA ACACAGTAAT TGCCTTACAT	5460
GACTTGAAAG ATATGGACTG GATATTCTAT CAGTAGCAGT ATTGTTACTT CTTTCCAGGA	5520

TGCAAGGTCT ATTATCCAA CAGAAGAAAA ATATTTTGT ATTTAAAGTT TATGCTGCAC	5580
TGTGCTGCAA ATGTTGTGGC ACTTTTTTT TAAGAAATGG AAGATGTTA CTTTTACAGG	5640
GACCTCAACA CTGCCCTTT CAGACTGGAT CTTACTATAA AACTCTTCAT GTCAAAGTGG	5700
TTCTAGGCTG AACACAGATT AAATTATGTT TGTAATGAA CACTTAAACA CTGACCTGTG	5760
CTTATGTTTC AGGAAAGAAT GGGGGATTAA TTTTGTTTA TTTCTTGGTA GAGAACTCTC	5820
AAGGACTTTG TTCACTTCC AAAGCTACTT GTTTACATTG TACACTGCGA CCACCTTGCC	5880
GCTTTCATC ACAAGCTTGA ATATTTAAAT TCTGTACCTA CAGTTGTAAA ATAGCCAGGA	5940
TTTCTCCTGT TTGTGATCAG TTATAATGCC TTTTATGAA ACAAACAAAC AAACAAAAAA	6000
CAATTAAAAA AAAAACACA ACAAAACCAA CAAATGGCTG TAAATTATTG TAAATTAAATT	6060
AAATGAGCTT TTTTCCGTCA GGCTTTTTT GGCTGTTCT TTCCCCAACAA ACTCAGGCCT	6120
TCTTTCACCA AAGTCAGTAT ACTTACATGT TTTAATAAAAA TATCTCGATG GAATCAGAAT	6180
GTAAAAATGG GGAAGGGAAT ATTTTATTCC ATTTAGTGCT CCTTTTTAT TGGATACTTT	6240
TACATACCTG TTTTGGTTG TTTTATTTA TTTTTTTT CTATTAAACT GTCAGTGTG	6300
TGATTGTTGT AATGAACAGT GAGAATATCC CACTCTAAC TGTGCCCTGG AAAGCTTTTC	6360
AGGTGCATTG GTTTAAAAGA AGGAAGTGTGTT CTATAGGTGA ACACCTCAAA ACCCAGATCA	6420
GCCAAGATTC ATTGTAAATC CATTGTTTT CCCTCTTAA CATGGGCAAT AATGTCAAAT	6480
GTGCTATGCA GCAGTTAATA TTTAGAAGA TTTGAATGAC TTTATTAACA GAATTGTTAC	6540
AATGCACACT GATTGTACAT AGATAACTTC TATCTGACAA ATTAAATTAA CTAAAACCAA	6600
AAAAAACCC	6608

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Asp Glu Ile Val Ser Val Lys His Leu His Lys Lys Ile Lys Thr Glu

1 5 10 15

Lys Glu Asn Glu Glu Lys Pro Glu Pro Asp Ile Gly Ile Lys Lys Glu

20 25 30

Ala Glu Glu Lys Arg Glu Thr Lys Glu Lys Glu Asn Lys Arg Glu Leu

35 40 45

Lys Arg Glu Lys Lys Glu Lys Glu Asp Lys Lys Glu Leu Lys Glu Lys

50 55 60

Asp Asn Lys Glu Lys Arg Glu Asn Lys Val Lys Glu Ser Thr Gln Lys

65 70 75 80

Glu Lys Glu Val Lys Glu Glu Lys

85

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 265 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GATGAGATTG TTTCA GTGAA ACATCTACAT AAAAAAATAA AAACAGAAAA AAGAAAATGA

60

AGAAAAGCCT GAGCCAGATA TTGGTATAAA GAAGGAAGCT GAAGAAAAAA GAGAGACAAA	120
AGAGAAGGAA AATAAAAGGG AATTGAAAAG GGAGAAAAAA GAAAAAGAGG ATAAGAAAGA	180
ATTAAAAGAA AAAGATAATA AAGAAAAGAG AGAAAACAAA GTAAAAGAAT CCACACAGAA	240
AGAAAAGAA GTGAAGGAAG AGAAG	265

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GATGGGATTG TTTCA GTGAA ACATCCACAT AAAAAAATAA AAGCAGAAAA AAGAAAATGA	60
AGAAAAGAT GAGCCAGAGA TTGGTATAAA GAAGGAAGCT GGAGAAAAAA GAGAGACAAA	120
AGAAAAGGAA AATAAGA	137

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Asp Gly Ile Val Ser Val Lys His Pro His Lys Lys Ile Lys Ala Glu
1 5 10 15
Lys Glu Asn Glu Glu Lys Asp Glu Pro Glu Ile Gly Ile Lys Lys Glu
20 25 30
Ala Gly Glu Lys Arg Glu Thr Lys Glu Lys Glu Asn Lys
35 40 45

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ATTTATCGGC TAGTCACAAA AGGATCAGTA GAAGAAGATA TTCTTGAAAG AGCCAAGAAA	60
AAGATGGTGT TAGATCATTT AGTGATTCAAG AGAATGGACA CCACAGGGAA AACTGTACTA	120
CATACAGGCT CTACTCCCTTC AAGCTCAACA CCTTTAATA AGGAAGAGTT ATCAGCAATT	180
TTGAAGTTG GTGCTGAGGA ACTTTTAAA GAACCTGAAN NNGAAGAAGA GGAGCCTCAG	240
GAGATGGATA TAGATGAAAT CCTGAAGAGG NCTGAAACTC GAGAAAATGA GTCAGGCCA	300
TTAACTGTAG GAGATGAGTT ACTTTCACAG TTCAAGGTAG CTAACCTTTC CAATATGGAT	360
GAAGATGACA TTGAATTGGA ACCAGAACAA AATCTAAGAA ACTGGGAAGA AATCATTCCA	420
GAAGTTCACT GGCGACGAAT AGAGGGGNNG GAAAGACAAA AAGAACTTGA AGAAATATAT	480
ATGCTTCAA GAATGAGAAA CTGTGCAAAA CAGATCAGCT TTAATGGAAA TGAAGGGAGA	540

TGCAGTAGGA GCAGAAGATA TTCTGGATCT GATACTGATT CCATCTCAGA AAGAAAACGA	600
CCAAAAAAAC GTGGACGACC ACGAACTATT CCCC GTGAAA ACATTAAAGG ATTTAGTGAT	660
GCAGAGATTA GACGATTTAT CAAGAGTTAC AAGAAATTG GTGGCCCAGT TGAAAGGTAA	720
GATGCTATAG CTAGAGATGC TGAGCTAGTT GATAAACTG AAACAGACCT TAGACGTCTG	780
GGAGAACATTG TACATAATGG ATGCATTAAG GCTTTAAATG ATAATGACTT TGGTCAAGGA	840
AGAACAGGTG GTAGATTGG GAAAGTTAAA GGCCCAACAT TCCGAATAGC AGGAGTGCAG	900
GTGAATGCAA AGCTAGTCAT TTCTCACGAA GAAGAGTTGG CACCATTGCA TAAATCGATT	960
CCTTCAGATC CAGAAGAAAG GAAAAGATAT GTCATCCCAT ACCACACCAA AGCAGCTCAT	1020
TTTGATATAG ATTGGGGTAA AGAAGATGAT TCCAATCTGT TAATAGGCAT CTATGAATAT	1080
GGTTATGGCA GTTGGGAAAT GATAAAAATG GATCCTGATC TCAGTTGAC ACAGAAGATT	1140
TTACCTGATG ATCCAGATAA GAAACCCAG GCTAAGCAGT TACAGACTCG TGCAGATTAC	1200
CTCATTAAAT TACTGAATAA AGACCTTGCA AGAAAGGAAG CACAGAGACT TGCTGGTGCA	1260
GGCAATTCAA AGAGGAGAAA AACAAAGAAGT AAGAAGAATA AAGCAACAAA GGCTGC	1316

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Asp Ala Arg Arg Tyr Leu Gly Lys Asn Leu Gly His Leu Arg Ile Ala

1 5 10 15

Ser Gln Thr His Tyr Phe Glu Asn Ile Arg Ser Thr Arg Lys Gly Ile

20	25	30
Leu Asp Leu His Leu Val Thr Val Asp Phe Leu Phe Asn Phe Leu Ile		
35	40	45
Leu Thr Met Asn Gly His Ser Asp Glu Glu Ser Val Arg Asn Ser Ser		
50	55	60
Gly Glu Ser Ser Arg Ser Asp Asp Asp Ser Ala Gly Ser Ala Ser Gly		
65	70	75
Ser Gly Ser Gly Ser Ser Ser Gly Ser Ser Ser Asp Gly Ser Ser Ser		
85	90	95
Gln Ser Gly Ser Ser Asp Ser Glu Ser Gly Ser Glu Ser Gly Ser Gln		
100	105	110
Ser Glu Ser Glu Ser Asp Thr Ser Arg Glu Lys Lys Gln Val Gln Ala		
115	120	125
Lys Pro Pro Lys Ala Asp Gly Ser Glu Phe Trp Lys Ser Ser Pro Ser		
130	135	140
Ile Leu Ala Val Gln Arg Ser Ala Val Leu Lys Lys Gln Gln Gln		
145	150	155
Gln Lys Ala Ala Ser Ser Asp Ser Gly Ser Glu Glu Asp Ser Ser Ser		
165	170	175
Ser Glu Asp Ser Ala Asp Asp Ser Ser Ser Glu Thr Lys Lys Lys		
180	185	190
His Lys Asp Glu Asp Trp Gln Met Ser Gly Ser Gly Ser Val Ser Gly		
195	200	205
Thr Gly Ser Asp Ser Glu Ser Ala Glu Asp Gly Asp Lys Ser Ser Cys		
210	215	220

Glu Glu Ser Glu Ser Asp Tyr Glu Pro Lys Asn Lys Val Lys Ser Arg
225 230 235 240
Lys Pro Pro Ser Arg Ile Lys Pro Lys Ser Gly Lys Lys Ser Thr Gly
245 250 255
Gln Lys Lys Arg Gln Leu Asp Ser Ser Glu Glu Glu Asp Asp Asp
260 265 270
Glu Asp Tyr Asp Lys Arg Gly Ser Arg Arg Gln Ala Thr Val Asn Val
275 280 285
Ser Tyr Lys Glu Ala Glu Glu Thr Lys Thr Asp Ser Asp Asp Leu Leu
290 295 300
Glu Val Cys Gly Glu Asp Val Pro Gln Thr Glu Glu Asp Glu Phe Glu
305 310 315 320
Thr Ile Glu Lys Phe Met Asp Ser Arg Ile Gly Arg Lys Gly Ala Thr
325 330 335
Gly Ala Ser Thr Thr Ile Tyr Ala Val Glu Ala Asp Gly Asp Pro Asn
340 345 350
Ala Gly Phe Glu Lys Ser Lys Glu Leu Gly Glu Ile Gln Tyr Leu Ile
355 360 365
Lys Trp Lys Gly Trp Ser His Ile His Asn Thr Trp Glu Thr Glu Glu
370 375 380
Thr Leu Lys Gln Gln Asn Val Lys Gly Met Asn Lys Leu Asp Asn Tyr
385 390 395 400
Lys Lys Lys Asp Gln Glu Thr Lys Arg Trp Leu Lys Asn Ala Ser Pro
405 410 415
Glu Asp Val Glu Tyr Tyr Asn Cys Gln Gln Glu Leu Thr Asp Asp Leu

420	425	430
His Lys Gln Tyr Gln Ile Val Glu Arg Ile Ile Ala His Ser Asn Gln		
435	440	445
Lys Ser Ala Ala Gly Tyr Pro Asp Tyr Tyr Cys Lys Trp Gln Gly Leu		
450	455	460
Pro Tyr Ser Glu Cys Ser Trp Glu Asp Gly Ala Leu Ile Ala Lys Lys		
465	470	475
Phe Gln Ala Arg Ile Asp Glu Tyr Phe Ser Arg Asn Gln Ser Lys Thr		
485	490	495
Thr Pro Phe Lys Asp Cys Lys Val Leu Lys Gln Arg Pro Arg Phe Val		
500	505	510
Ala Leu Lys Lys Gln Pro Ser Tyr Ile Gly Gly His Glu Ser Leu Glu		
515	520	525
Leu Arg Asp Tyr Gln Leu Asn Gly Leu Asn Trp Leu Ala His Ser Trp		
530	535	540
Cys Lys Gly Asn Ser Cys Ile Leu Ala Asp Glu Met Gly Leu Gly Lys		
545	550	555
Thr Ile Gln Thr Ile Ser Phe Leu Asn Tyr Leu Phe His Glu His Gln		
565	570	575
Leu Tyr Gly Pro Phe Leu Leu Arg Val Pro Leu Ser Thr Leu Thr Ser		
580	585	590
Trp Gln Arg Glu Ile Gln Thr Trp Ala Pro Gln Met Asn Ala Val Val		
595	600	605
Tyr Leu Gly Asp Ile Thr Ser Arg Asn Met Ile Arg Thr His Glu Trp		
610	615	620

Met His Pro Gln Thr Lys Arg Leu Lys Phe Asn Ile Leu Leu Thr Thr
625 630 635 640
Tyr Glu Ile Leu Leu Lys Asp Lys Ser Phe Leu Gly Gly Leu Asn Trp
645 650 655
Ala Phe Ile Gly Val Asp Glu Ala His Arg Leu Lys Asn Asp Asp Ser
660 665 670
Leu Leu Tyr Arg Thr Leu Ile Asp Phe Lys Ser Asn His Arg Leu Leu
675 680 685
Ile Thr Gly Thr Pro Leu Gln Asn Ser Leu Lys Glu Leu Trp Ser Leu
690 695 700
Leu His Phe Ile Met Pro Glu Lys Phe Ser Ser Trp Glu Asp Phe Glu
705 710 715 720
Glu Glu His Gly Lys Gly Arg Glu Tyr Gly Tyr Ala Ser Leu His Lys
725 730 735
Glu Leu Glu Pro Phe Leu Leu Arg Arg Val Lys Lys Asp Val Glu Lys
740 745 750
Ser Leu Pro Ala Lys Val Glu Gln Ile Leu Arg Met Glu Met Ser Ala
755 760 765
Leu Gln Lys Gln Tyr Tyr Lys Trp Ile Leu Thr Arg Asn Tyr Lys Ala
770 775 780
Leu Ser Lys Gly Ser Lys Gly Ser Thr Ser Gly Phe Leu Asn Ile Met
785 790 795 800
Met Glu Leu Lys Lys Cys Cys Asn His Cys Tyr Leu Ile Lys Pro Pro
805 810 815
Asp Asp Asn Glu Phe Tyr Asn Lys Gln Glu Ala Leu Gln His Leu Ile

820 825 830
Arg Ser Ser Gly Lys Leu Ile Leu Leu Asp Lys Leu Leu Ile Arg Leu
835 840 845
Arg Glu Arg Gly Asn Arg Val Leu Ile Phe Ser Gln Met Val Arg Met
850 855 860
Leu Asp Ile Leu Ala Glu Tyr Leu Lys Tyr Arg Gln Phe Pro Phe Gln
865 870 875 880
Arg Leu Asp Gly Ser Ile Lys Gly Glu Leu Arg Lys Gln Ala Leu Asp
885 890 895
His Phe Asn Ala Glu Gly Ser Glu Asp Phe Cys Phe Leu Leu Ser Thr
900 905 910
Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala Ser Ala Asp Thr Val Val
915 920 925
Ile Phe Asp Ser Asp Trp Asn Pro Gln Asn Asp Leu Gln Ala Gln Ala
930 935 940
Arg Ala His Arg Ile Gly Gln Lys Lys Gln Val Asn Ile Tyr Arg Leu
945 950 955 960
Val Thr Lys Gly Ser Val Glu Glu Asp Ile Leu Glu Arg Ala Lys Lys
965 970 975
Lys Met Val Leu Asp His Leu Val Ile Gln Arg Met Asp Thr Thr Gly
980 985 990
Lys Thr Val Leu His Thr Gly Ser Ala Pro Ser Ser Thr Pro Phe
995 1000 1005
Asn Lys Glu Glu Leu Ser Ala Ile Leu Lys Phe Gly Ala Glu Glu Leu
1010 1015 1020

Phe Lys Glu Pro Glu Gly Glu Glu Gln Glu Pro Gln Glu Met Asp Ile
1025 1030 1035 1040
Asp Glu Ile Leu Lys Arg Ala Glu Thr His Glu Asn Glu Pro Gly Pro
 1045 1050 1055
Leu Ser Val Gly Asp Glu Leu Leu Ser Gln Phe Lys Val Ala Asn Phe
 1060 1065 1070
Ser Asn Met Asp Glu Asp Asp Ile Glu Leu Glu Pro Glu Arg Asn Ser
 1075 1080 1085
Lys Asn Trp Glu Glu Ile Ile Pro Glu Glu Gln Arg Arg Arg Leu Glu
 1090 1095 1100
Glu Glu Glu Arg Gln Lys Glu Leu Glu Glu Ile Tyr Met Leu Pro Arg
1105 1110 1115 1120
Met Arg Asn Cys Ala Lys Gln Ile Ser Phe Asn Gly Ser Glu Gly Arg
 1125 1130 1135
Arg Ser Arg Ser Arg Arg Tyr Ser Gly Ser Asp Ser Asp Ser Ile Ser
 1140 1145 1150
Glu Arg Lys Arg Pro Lys Lys Arg Gly Arg Pro Arg Thr Ile Pro Arg
 1155 1160 1165
Glu Asn Ile Lys Gly Phe Ser Asp Ala Glu Ile Arg Arg Phe Ile Lys
 1170 1175 1180
Ser Tyr Lys Lys Phe Gly Gly Pro Leu Glu Arg Leu Asp Ala Ile Ala
1185 1190 1195 1200
Arg Asp Ala Glu Leu Val Asp Lys Ser Glu Thr Asp Leu Arg Arg Leu
 1205 1210 1215
Gly Glu Leu Val His Asn Gly Cys Val Lys Ala Leu Lys Asp Ser Ser

1220	1225	1230
Ser Gly Thr Glu Arg Ala Gly Gly Arg Leu Gly Lys Val Lys Gly Pro		
1235	1240	1245
Thr Phe Arg Ile Ser Gly Val Gln Val Asn Ala Lys Leu Val Ile Ala		
1250	1255	1260
His Glu Asp Glu Leu Ile Pro Leu His Lys Ser Ile Pro Ser Asp Pro		
1265	1270	1275
Glu Glu Arg Lys Gln Tyr Thr Ile Pro Cys His Thr Lys Ala Ala His		
1285	1290	1295
Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn Leu Leu Ile Gly		
1300	1305	1310
Ile Tyr Glu Tyr Gly Tyr Gly Ser Trp Glu Met Ile Lys Met Asp Pro		
1315	1320	1325
Asp Leu Ser Leu Thr His Lys Ile Leu Pro Asp Asp Pro Asp Lys Lys		
1330	1335	1340
Pro Gln Ala Lys Gln Leu Gln Thr Arg Ala Asp Tyr Leu Ile Lys Leu		
1345	1350	1355
Leu Ser Arg Asp Leu Ala Lys Arg Glu Ala Gln Arg Leu Cys Gly Ala		
1365	1370	1375
Gly Gly Ser Lys Arg Arg Lys Thr Arg Ala Lys Lys Ser Lys Ala Met		
1380	1385	1390
Lys Ser Ile Lys Val Lys Glu Glu Ile Lys Ser Asp Ser Ser Pro Leu		
1395	1400	1405
Pro Ser Glu Lys Ser Asp Glu Asp Asp Asp Lys Leu Asn Asp Ser Lys		
1410	1415	1420

Pro Glu Ser Lys Asp Arg Ser Lys Lys Ser Val Val Ser Asp Ala Pro
1425 1430 1435 1440
Val His Ile Thr Ala Ser Gly Glu Pro Val Pro Ile Ala Glu Glu Ser
 1445 1450 1455
Glu Glu Leu Asp Gln Lys Thr Phe Ser Ile Cys Lys Glu Arg Met Arg
 1460 1465 1470
Pro Val Lys Ala Ala Leu Lys Gln Leu Asp Arg Pro Glu Lys Gly Leu
1475 1480 1485
Ser Glu Arg Glu Gln Leu Glu His Thr Arg Gln Cys Leu Ile Lys Ile
1490 1495 1500
Gly Asp His Ile Thr Glu Cys Leu Lys Glu Tyr Ser Asn Pro Glu Gln
1505 1510 1515 1520
Ile Lys Gln Trp Arg Lys Asn Leu Trp Ile Phe Val Ser Lys Phe Thr
 1525 1530 1535
Glu Phe Asp Ala Arg Lys Leu His Lys Leu Tyr Lys His Ala Ile Lys
 1540 1545 1550
Lys Arg Gln Glu Ser Gln Gln Asn Ser Asp Gln Asn Ser Asn Val Ala
 1555 1560 1565
Thr Thr His Val Ile Arg Asn Pro Asp Met Glu Arg Leu Lys Glu Asn
 1570 1575 1580
Thr Asn His Asp Asp Ser Ser Arg Asp Ser Tyr Ser Ser Asp Arg His
1585 1590 1595 1600
Leu Ser Gln Tyr His Asp His His Lys Asp Arg His Gln Gly Asp Ser
 1605 1610 1615
Tyr Lys Lys Ser Asp Ser Arg Lys Arg Pro Tyr Ser Ser Phe Ser Asn

1620 1625 1630
Gly Lys Asp His Arg Glu Trp Asp His Tyr Arg Gln Asp Ser Arg Tyr
1635 1640 1645
Tyr Ser Asp Arg Glu Lys His Arg Lys Leu Asp Asp His Arg Ser Arg
1650 1655 1660
Glu His Arg Pro Ser Leu Glu Gly Gly Leu Lys Asp Leu Asp Gln Arg
1665 1670 1675 1680
Ser Pro Tyr Gly Ser Arg Ser Pro Phe Glu His Ser Ala Glu His Arg
1685 1690 1695
Ser Thr Pro Glu His Thr Trp Ser Ser Arg Lys Thr Xaa Gln Lys Leu
1700 1705 1710
Met Ser Leu Ser Ser Gly Thr Leu Phe Xaa Pro Leu Thr Xaa Leu Glu
1715 1720 1725
Arg Tyr Gly Leu Asp Ile Leu Ser Val Ala Val Leu Leu Leu Ser
1730 1735 1740
Arg Met Gln Gly Leu Leu Ser Gln Gln Lys Lys Asn Ile Phe Val Phe
1745 1750 1755 1760
Lys Val Tyr Ala Ala Leu Cys Cys Lys Cys Cys Gly Thr Phe Phe Leu
1765 1770 1775
Arg Asn Gly Arg Cys Leu Leu Gln Gly Pro Gln His Cys Pro Phe
1780 1785 1790
Gln Thr Gly Ser Tyr Tyr Lys Thr Leu His Val Lys Val Val Leu Gly
1795 1800 1805
Xaa Thr Gln Ile Lys Leu Cys Leu Xaa Met Asn Thr Xaa Thr Leu Thr
1810 1815 1820

Cys Ala Tyr Val Ser Gly Lys Asn Gly Gly Phe Ile Leu Phe Tyr Phe
1825 1830 1835 1840
Leu Val Glu Asn Ser Gln Gly Leu Cys Ser Leu Ser Lys Ala Thr Cys
1845 1850 1855
Leu His Cys Thr Leu Arg Pro Pro Cys Arg Phe Ser Ser Gln Ala Xaa
1860 1865 1870
Ile Phe Lys Phe Cys Thr Tyr Ser Cys Lys Ile Ala Arg Ile Ser Pro
1875 1880 1885
Val Cys Asp Gln Leu Xaa Cys Leu Phe Met Lys Gln Thr Asn Lys Gln
1890 1895 1900
Lys Thr Ile Lys Lys Asn Thr Thr Lys Pro Thr Asn Gly Cys Lys
1905 1910 1915 1920
Leu Leu Xaa Ile Asn Xaa Met Ser Phe Phe Pro Ser Gly Phe Phe Trp
1925 1930 1935
Leu Phe Leu Ser Pro Thr Thr Gln Ala Phe Phe Ser Gln Ser Gln Tyr
1940 1945 1950
Thr Tyr Met Phe Xaa Xaa Asn Ile Ser Met Glu Ser Glu Cys Lys Asn
1955 1960 1965
Gly Glu Gly Asn Ile Leu Phe His Leu Val Leu Leu Phe Tyr Trp Ile
1970 1975 1980
Leu Leu His Thr Cys Phe Trp Leu Phe Tyr Phe Ile Phe Phe Tyr
1985 1990 1995 2000
Xaa Thr Val Ser Val Val Ile Val Val Met Asn Ser Glu Asn Ile Pro
2005 2010 2015
Leu Xaa Thr Val Pro Trp Lys Ala Phe Gln Val His Trp Phe Lys Arg

2020	2025	2030
Arg Lys Cys Ser Ile Gly Glu His Phe Lys Thr Gln Ile Ser Gln Asp		
2035	2040	2045
Ser Leu Xaa Ile His Leu Phe Ser Leu Phe Asn Met Gly Asn Asn Val		
2050	2055	2060
Lys Cys Ala Met Gln Gln Leu Ile Phe Xaa Lys Ile Xaa Met Thr Leu		
2065	2070	2075
Leu Thr Glu Leu Leu Gln Cys Thr Leu Ile Val His Arg Xaa Leu Leu		
2085	2090	2095
Ser Asp Lys Leu Asn Xaa Leu Lys Pro Lys Lys Thr		
2100	2105	

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1795 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Phe Ala Leu Cys Pro Pro Val Thr Gln Arg Glu Pro Gln Glu Thr Arg

1 5 10 15

Glu Cys Arg Lys Phe Ile Phe Glu Ile Leu Ile Phe Glu Glu Ile Cys

20 25 30

Ile His Thr His Leu Leu Leu Ile Gly Asp Phe Cys Phe Ile Asn Phe

35	40	45
Leu Ile Phe Thr Met Asn Gly His Ser Asp Glu Glu Ser Val Arg Asn		
50	55	60
Gly Ser Gly Glu Ser Ser Gln Ser Gly Asp Asp Cys Gly Ser Ala Ser		
65	70	75
Gly Ser Gly Ser Gly Ser Ser Ser Gly Ser Ser Ser Asp Gly Ser Ser		
85	90	95
Ser Gln Ser Gly Ser Ser Asp Ser Asp Ser Gly Ser Asp Ser Gly Ser		
100	105	110
Gln Ser Glu Ser Glu Ser Asp Thr Ser Arg Glu Asn Lys Val Gln Ala		
115	120	125
Lys Pro Pro Lys Val Asp Gly Ala Glu Phe Trp Lys Ser Ser Pro Ser		
130	135	140
Ile Leu Ala Val Gln Arg Ser Ala Met Leu Arg Lys Gln Pro Gln Gln		
145	150	155
Ala Gln Gln Gln Arg Pro Ala Ser Ser Asn Ser Gly Ser Glu Glu Asp		
165	170	175
Ser Ser Ser Ser Glu Asp Ser Asp Asp Ser Ser Ser Gly Ala Lys Arg		
180	185	190
Lys Lys His Asn Asp Glu Asp Trp Gln Met Ser Gly Ser Gly Ser Pro		
195	200	205
Ser Gln Leu Gly Ser Asp Ser Glu Ser Glu Glu Glu Arg Asp Lys Ser		
210	215	220
Ser Cys Asp Gly Thr Glu Ser Asp Tyr Glu Pro Lys Asn Lys Val Arg		
225	230	235
240		

Ser Arg Lys Pro Gln Asn Arg Ser Lys Ser Lys Asn Gly Lys Lys Ile
245 250 255
Leu Gly Gln Lys Lys Arg Gln Ile Asp Ser Ser Glu Asp Glu Asp Asp
260 265 270
Glu Asp Tyr Asp Asn Asp Lys Arg Ser Ser Arg Arg Gln Ala Thr Val
275 280 285
Asn Val Ser Tyr Lys Glu Asp Glu Glu Met Lys Thr Asp Ser Asp Asp
290 295 300
Leu Leu Glu Val Cys Gly Glu Asp Val Pro Gln Pro Glu Asp Glu Glu
305 310 315 320
Phe Glu Thr Ile Glu Arg Val Met Asp Cys Arg Val Gly Arg Lys Gly
325 330 335
Ala Thr Gly Ala Thr Thr Ile Tyr Ala Val Glu Ala Asp Gly Asp
340 345 350
Pro Asn Ala Gly Phe Glu Arg Asn Lys Glu Pro Gly Asp Ile Gln Tyr
355 360 365
Leu Ile Lys Trp Lys Gly Trp Ser His Ile His Asn Thr Trp Glu Thr
370 375 380
Glu Glu Thr Leu Lys Gln Gln Asn Val Arg Gly Met Lys Lys Leu Asp
385 390 395 400
Asn Tyr Lys Lys Asp Gln Glu Thr Lys Arg Trp Leu Lys Asn Ala
405 410 415
Ser Pro Glu Asp Val Glu Tyr Tyr Asn Cys Gln Gln Glu Leu Thr Asp
420 425 430
Asp Leu His Lys Gln Tyr Gln Ile Val Glu Arg Ile Ile Ala His Ser

435	440	445
Asn Gln Lys Ser Ala Ala Gly Leu Pro Asp Tyr Tyr Cys Lys Trp Gln		
450	455	460
Gly Leu Pro Tyr Ser Glu Cys Ser Trp Glu Asp Gly Ala Leu Ile Ser		
465	470	475
480		
Lys Lys Phe Gln Thr Cys Ile Asp Glu Tyr Phe Ser Arg Asn Gln Ser		
485	490	495
Lys Thr Thr Pro Phe Lys Asp Cys Lys Val Leu Lys Gln Arg Pro Arg		
500	505	510
Phe Val Ala Leu Lys Lys Gln Pro Ser Tyr Ile Gly Gly His Glu Gly		
515	520	525
Leu Glu Leu Arg Asp Tyr Gln Leu Asn Gly Leu Asn Trp Leu Ala His		
530	535	540
Ser Trp Cys Lys Gly Asn Ser Cys Ile Leu Ala Asp Glu Met Gly Leu		
545	550	555
560		
Gly Lys Thr Ile Gln Thr Ile Ser Phe Leu Asn Tyr Leu Phe His Glu		
565	570	575
His Gln Leu Tyr Gly Pro Phe Leu Leu Val Val Pro Leu Ser Thr Leu		
580	585	590
Thr Ser Trp Gln Arg Glu Ile Gln Thr Trp Ala Ser Gln Met Asn Ala		
595	600	605
Val Val Tyr Leu Gly Asp Ile Asn Ser Arg Asn Met Ile Arg Thr His		
610	615	620
Glu Trp Met His Pro Gln Thr Lys Arg Leu Lys Phe Asn Ile Leu Leu		
625	630	635
640		

Thr Thr Tyr Glu Ile Leu Leu Lys Asp Lys Ala Phe Leu Gly Gly Leu
645 650 655
Asn Trp Ala Phe Ile Gly Val Asp Glu Ala His Arg Leu Lys Asn Asp
660 665 670
Asp Ser Leu Leu Tyr Lys Thr Leu Ile Asp Phe Lys Ser Asn His Arg
675 680 685
Leu Leu Ile Thr Gly Thr Pro Leu Gln Asn Ser Leu Lys Glu Leu Trp
690 695 700
Ser Leu Leu His Phe Ile Met Pro Glu Lys Phe Ser Ser Trp Glu Asp
705 710 715 720
Phe Glu Glu Glu His Gly Lys Gly Arg Glu Tyr Gly Tyr Ala Ser Leu
725 730 735
His Lys Glu Leu Glu Pro Phe Leu Leu Arg Arg Val Lys Lys Asp Val
740 745 750
Glu Lys Ser Leu Pro Ala Lys Val Glu Gln Ile Leu Arg Met Glu Met
755 760 765
Ser Ala Leu Gln Lys Gln Tyr Tyr Lys Trp Ile Leu Thr Arg Asn Tyr
770 775 780
Lys Ala Leu Ser Lys Gly Ser Lys Gly Ser Thr Ser Gly Phe Leu Asn
785 790 795 800
Ile Met Met Glu Leu Lys Lys Cys Cys Asn His Cys Tyr Leu Ile Lys
805 810 815
Pro Pro Asp Asn Asn Glu Phe Tyr Asn Lys Gln Glu Ala Leu Gln His
820 825 830
Leu Ile Arg Ser Ser Gly Lys Leu Ile Leu Leu Asp Lys Leu Leu Ile

835

840

845

Arg Leu Arg Glu Arg Gly Asn Arg Val Leu Ile Phe Ser Gln Met Val

850

855

860

Arg Met Leu Asp Ile Leu Ala Glu Tyr Leu Lys Tyr Arg Gln Phe Pro

865

870

875

880

Phe Gln Arg Leu Asp Gly Ser Ile Lys Gly Glu Leu Arg Lys Gln Ala

885

890

895

Leu Asp His Phe Asn Ala Glu Gly Ser Glu Asp Phe Cys Phe Leu Leu

900

905

910

Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala Ser Ala Asp Thr

915

920

925

Val Val Ile Phe Asp Ser Asp Trp Asn Pro Gln Asn Asp Leu Gln Ala

930

935

940

Gln Ala Arg Ala His Arg Ile Gly Gln Lys Lys Gln Val Asn Ile Tyr

945

950

955

960

Arg Leu Val Thr Lys Gly Ser Val Glu Glu Asp Ile Leu Glu Arg Ala

965

970

975

Lys Lys Lys Met Val Leu Asp His Leu Val Ile Gln Arg Met Asp Thr

980

985

990

Thr Gly Lys Thr Val Leu His Thr Gly Ser Thr Pro Ser Ser Ser Thr

995

1000

1005

Pro Phe Asn Lys Glu Glu Leu Ser Ala Ile Leu Lys Phe Gly Ala Glu

1010

1015

1020

Glu Leu Phe Lys Glu Pro Glu Gly Glu Glu Gln Glu Pro Gln Glu Met

1025

1030

1035

1040

Asp Ile Asp Glu Ile Leu Lys Arg Ala Glu Thr Arg Glu Asn Glu Pro
1045 1050 1055
Gly Pro Leu Thr Val Gly Asp Glu Leu Leu Ser Gln Phe Lys Val Ala
1060 1065 1070
Asn Phe Ser Asn Met Asp Glu Asp Asp Ile Glu Leu Glu Pro Glu Arg
1075 1080 1085
Asn Ser Arg Asn Trp Glu Glu Ile Ile Pro Glu Ser Gln Arg Arg Arg
1090 1095 1100
Ile Glu Glu Glu Glu Arg Gln Lys Glu Leu Glu Glu Ile Tyr Met Leu
1105 1110 1115 1120
Pro Arg Met Arg Asn Cys Ala Lys Gln Ile Ser Phe Asn Gly Ser Glu
1125 1130 1135
Gly Arg Arg Ser Arg Ser Arg Arg Tyr Ser Gly Ser Asp Ser Asp Ser
1140 1145 1150
Ile Thr Glu Arg Lys Arg Pro Lys Lys Arg Gly Arg Pro Arg Thr Ile
1155 1160 1165
Pro Arg Glu Asn Ile Lys Gly Phe Ser Asp Ala Glu Ile Arg Arg Phe
1170 1175 1180
Ile Lys Ser Tyr Lys Lys Phe Gly Gly Pro Leu Glu Arg Leu Asp Ala
1185 1190 1195 1200
Val Ala Arg Asp Ala Glu Leu Val Asp Lys Ser Glu Thr Asp Leu Arg
1205 1210 1215
Arg Leu Gly Glu Leu Val His Asn Gly Cys Ile Lys Ala Leu Lys Asp
1220 1225 1230
Asn Ser Ser Gly Gln Glu Arg Ala Gly Gly Arg Leu Gly Lys Val Lys

1235 1240 1245
Gly Pro Thr Phe Arg Ile Ser Gly Val Gln Val Asn Ala Lys Leu Val
1250 1255 1260
Ile Ser His Glu Glu Glu Leu Ala Pro Leu His Lys Ser Ile Pro Ser
1265 1270 1275 1280
Asp Pro Glu Glu Arg Lys Arg Tyr Val Ile Pro Cys His Thr Lys Ala
1285 1290 1295
Ala His Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn Leu Leu
1300 1305 1310
Val Gly Ile Tyr Glu Tyr Gly Tyr Gly Ser Trp Glu Met Ile Lys Met
1315 1320 1325
Asp Pro Asp Leu Ser Leu Thr Gln Lys Ile Leu Pro Asp Asp Pro Asp
1330 1335 1340
Lys Lys Pro Gln Ala Lys Gln Leu Gln Thr Arg Ala Asp Tyr Leu Ile
1345 1350 1355 1360
Lys Leu Leu Asn Lys Asp Leu Ala Arg Lys Glu Ala Gln Arg Leu Ala
1365 1370 1375
Gly Ala Gly Asn Ser Lys Arg Arg Lys Thr Arg Asn Lys Lys Asn Lys
1380 1385 1390
Met Lys Ala Ser Lys Ile Lys Glu Glu Ile Lys Ser Asp Ser Ser Pro
1395 1400 1405
Gln Pro Ser Glu Lys Ser Asp Glu Asp Asp Glu Glu Asp Asn Lys
1410 1415 1420
Val Asn Glu Met Lys Ser Glu Asn Lys Glu Lys Ser Lys Lys Ile Pro
1425 1430 1435 1440

Leu Leu Asp Thr Pro Val His Ile Thr Ala Thr Ser Glu Pro Val Pro
1445 1450 1455
Ile Ser Glu Glu Ser Glu Glu Leu His Gln Lys Thr Phe Ser Val Cys
1460 1465 1470
Lys Glu Arg Met Arg Pro Val Lys Ala Ala Leu Lys Gln Leu Asp Arg
1475 1480 1485
Pro Glu Lys Gly Leu Ser Glu Arg Glu Gln Leu Glu His Thr Arg Gln
1490 1495 1500
Cys Leu Ile Lys Ile Gly Asp His Ile Thr Glu Cys Leu Lys Glu Tyr
1505 1510 1515 1520
Thr Asn Pro Glu Gln Ile Lys Gln Trp Arg Lys Asn Leu Trp Ile Phe
1525 1530 1535
Val Ser Lys Phe Thr Glu Phe Asp Ala Arg Lys Leu His Lys Leu Tyr
1540 1545 1550
Lys His Ala Ile Lys Lys Arg Gln Glu Ser Gln Gln His Asn Asp Gln
1555 1560 1565
Asn Ile Ser Ser Asn Val Asn Thr His Val Ile Arg Asn Pro Asp Val
1570 1575 1580
Glu Arg Leu Lys Glu Thr Thr Asn His Asp Asp Ser Ser Arg Asp Ser
1585 1590 1595 1600
Tyr Ser Ser Asp Arg His Leu Ser Gln Tyr His Asp His His Lys Asp
1605 1610 1615
Arg His Gln Gly Asp Ala Tyr Lys Ser Asp Ser Arg Lys Arg Pro
1620 1625 1630
Tyr Ser Ala Phe Ser Asn Gly Lys Asp His Arg Asp Trp Asp His Tyr

1635 1640 1645
Lys Gln Asp Ser Arg Tyr Tyr Ser Asp Ser Lys His Arg Lys Leu Asp
1650 1655 1660
Asp His Arg Ser Arg Asp His Arg Ser Asn Leu Glu Gly Asn Leu Lys
1665 1670 1675 1680
Asp Ser Arg Gly His Ser Asp His Arg Ser His Ser Asp His Arg Ile
1685 1690 1695
His Ser Asp His Arg Ser Thr Ser Glu Tyr Ser His His Lys Ser Ser
1700 1705 1710
Arg Asp Tyr Arg Tyr His Ser Asp Trp Gln Met Asp His Arg Ala Ser
1715 1720 1725
Gly Ser Gly Pro Arg Ser Pro Leu Asp Gln Arg Ser Pro Tyr Gly Ser
1730 1735 1740
Arg Ser Pro Leu Gly His Arg Ser Pro Phe Glu His Ser Ser Asp His
1745 1750 1755 1760
Lys Ser Thr Pro Glu His Thr Trp Ser Ser Arg Lys Thr Xaa Gln Arg
1765 1770 1775
Leu Thr Phe Ser Gly Pro Ser Phe Xaa Pro Tyr Thr Val Asn Xaa His
1780 1785 1790
Ser Asn Cys
1795

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Lys Thr Xaa Glu Pro Gly Glu Ile Gln Tyr Leu Ile Lys Trp Lys Gly

1 5 10 15

Trp Ser His Ile His Asn Thr Trp Glu Thr Glu Glu Thr Leu Lys Gln

20 25 30

Gln Asn Val Arg Gly Met Lys Lys Leu Asp Asn Tyr Lys Lys Lys Asp

35 40 45

Gln Glu Thr Lys Arg Trp Leu Lys Asn Ala Ser Pro Glu Asp Val Glu

50 55 60

Tyr Tyr Asn Cys Gln Gln Glu Leu Thr Asp Asp Leu His Lys Gln Tyr

65 70 75 80

Gln Ile Val Glu Arg Thr Asn Xaa Ser Phe Gln Ser Lys Ser Ala Ala

85 90 95

Gly Tyr Pro

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 439 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Ile Tyr Arg Leu Val Thr Lys Gly Ser Val Glu Glu Asp Ile Leu Glu
1 5 10 15
Arg Ala Lys Lys Lys Met Val Leu Asp His Leu Val Ile Gln Arg Met
20 25 30
Asp Thr Thr Gly Lys Thr Val Leu His Thr Gly Ser Thr Pro Ser Ser
35 40 45
Ser Thr Pro Phe Asn Lys Glu Glu Leu Ser Ala Ile Leu Lys Phe Gly
50 55 60
Ala Glu Glu Leu Phe Lys Glu Pro Glu Xaa Glu Glu Glu Pro Gln
65 70 75 80
Glu Met Asp Ile Asp Glu Ile Leu Lys Arg Xaa Glu Thr Arg Glu Asn
85 90 95
Glu Ser Gly Pro Leu Thr Val Gly Asp Glu Leu Leu Ser Gln Phe Lys
100 105 110
Val Ala Asn Phe Ser Asn Met Asp Glu Asp Asp Ile Glu Leu Glu Pro
115 120 125
Glu Gln Asn Leu Arg Asn Trp Glu Glu Ile Ile Pro Glu Val Gln Trp
130 135 140
Arg Arg Ile Glu Gly Xaa Glu Arg Gln Lys Glu Leu Glu Glu Ile Tyr
145 150 155 160
Met Leu Pro Arg Met Arg Asn Cys Ala Lys Gln Ile Ser Phe Asn Gly
165 170 175
Asn Glu Gly Arg Cys Ser Arg Ser Arg Arg Tyr Ser Gly Ser Asp Ser

180	185	190
Asp Ser Ile Ser Glu Arg Lys Arg Pro Lys Lys Arg Gly Arg Pro Arg		
195	200	205
Thr Ile Pro Arg Glu Asn Ile Lys Gly Phe Ser Asp Ala Glu Ile Arg		
210	215	220
Arg Phe Ile Lys Ser Tyr Lys Lys Phe Gly Gly Pro Val Glu Arg Leu		
225	230	235
Asp Ala Ile Ala Arg Asp Ala Glu Leu Val Asp Lys Ser Glu Thr Asp		
245	250	255
Leu Arg Arg Leu Gly Glu Leu Val His Asn Gly Cys Ile Lys Ala Leu		
260	265	270
Asn Asp Asn Asp Phe Gly Gln Gly Arg Thr Gly Gly Arg Phe Gly Lys		
275	280	285
Val Lys Gly Pro Thr Phe Arg Ile Ala Gly Val Gln Val Asn Ala Lys		
290	295	300
Leu Val Ile Ser His Glu Glu Glu Leu Ala Pro Leu His Lys Ser Ile		
305	310	315
Pro Ser Asp Pro Glu Glu Arg Lys Arg Tyr Val Ile Pro Tyr His Thr		
325	330	335
Lys Ala Ala His Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn		
340	345	350
Leu Leu Ile Gly Ile Tyr Glu Tyr Gly Tyr Ser Trp Glu Met Ile		
355	360	365
Lys Met Asp Pro Asp Leu Ser Leu Thr Gln Lys Ile Leu Pro Asp Asp		
370	375	380

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Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln Thr Arg Ala Asp Tyr
385 390 395 400
Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg Lys Glu Ala Gln Arg
405 410 415
Leu Ala Gly Ala Gly Asn Ser Lys Arg Arg Lys Thr Arg Ser Lys Lys
420 425 430
Asn Lys Ala Thr Lys Ala Ala
435

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1434 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..1434
- (D) OTHER INFORMATION:/note= "The sequence beginning at 1 corresponds to 55 and that ending at 1434 corresponds to 1488"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Lys Pro Pro Lys Ala Asp Gly Ser Glu Phe Trp Lys Ser Ser Pro Ser

1

5

10

15

Ile Leu Ala Val Gln Arg Ser Ala Val Leu Lys Lys Gln Gln Gln
20 25 30
Gln Lys Ala Ala Ser Ser Asp Ser Gly Ser Glu Glu Asp Ser Ser Ser
35 40 45
Ser Glu Asp Ser Ala Asp Asp Ser Ser Ser Glu Thr Lys Lys Lys Lys
50 55 60
His Lys Asp Glu Asp Trp Gln Met Ser Gly Ser Gly Ser Val Ser Gly
65 70 75 80
Thr Gly Ser Asp Ser Glu Ser Ala Glu Asp Gly Asp Lys Ser Ser Cys
85 90 95
Glu Glu Ser Glu Ser Asp Tyr Glu Pro Lys Asn Lys Val Lys Ser Arg
100 105 110
Lys Pro Pro Ser Arg Ile Lys Pro Lys Ser Gly Lys Lys Ser Thr Gly
115 120 125
Gln Lys Lys Arg Gln Leu Asp Ser Ser Glu Glu Glu Asp Asp Asp
130 135 140
Glu Asp Tyr Asp Lys Arg Gly Ser Arg Arg Gln Ala Thr Val Asn Val
145 150 155 160
Ser Tyr Lys Glu Ala Glu Glu Thr Lys Thr Asp Ser Asp Asp Leu Leu
165 170 175
Glu Val Cys Gly Glu Asp Val Pro Gln Thr Glu Glu Asp Glu Phe Glu
180 185 190
Thr Ile Glu Lys Phe Met Asp Ser Arg Ile Gly Arg Lys Gly Ala Thr
195 200 205
Gly Ala Ser Thr Thr Ile Tyr Ala Val Glu Ala Asp Gly Asp Pro Asn

210

215

220

Ala Gly Phe Glu Lys Ser Lys Glu Leu Gly Glu Ile Gln Tyr Leu Ile

225

230

235

240

Lys Trp Lys Gly Trp Ser His Ile His Asn Thr Trp Glu Thr Glu Glu

245

250

255

Thr Leu Lys Gln Gln Asn Val Lys Gly Met Asn Lys Leu Asp Asn Tyr

260

265

270

Lys Lys Lys Asp Gln Glu Thr Lys Arg Trp Leu Lys Asn Ala Ser Pro

275

280

285

Glu Asp Val Glu Tyr Tyr Asn Cys Gln Gln Glu Leu Thr Asp Asp Leu

290

295

300

His Lys Gln Tyr Gln Ile Val Glu Arg Ile Ile Ala His Ser Asn Gln

305

310

315

320

Lys Ser Ala Ala Gly Tyr Pro Asp Tyr Tyr Cys Lys Trp Gln Gly Leu

325

330

335

Pro Tyr Ser Glu Cys Ser Trp Glu Asp Gly Ala Leu Ile Ala Lys Lys

340

345

350

Phe Gln Ala Arg Ile Asp Glu Tyr Phe Ser Arg Asn Gln Ser Lys Thr

355

360

365

Thr Pro Phe Lys Asp Cys Lys Val Leu Lys Gln Arg Pro Arg Phe Val

370

375

380

Ala Leu Lys Lys Gln Pro Ser Tyr Ile Gly Gly His Glu Ser Leu Glu

385

390

395

400

Leu Arg Asp Tyr Gln Leu Asn Gly Leu Asn Trp Leu Ala His Ser Trp

405

410

415

Cys Lys Gly Asn Ser Cys Ile Leu Ala Asp Glu Met Gly Leu Gly Lys
420 425 430

Thr Ile Gln Thr Ile Ser Phe Leu Asn Tyr Leu Phe His Glu His Gln
435 440 445

Leu Tyr Gly Pro Phe Leu Leu Arg Val Pro Leu Ser Thr Leu Thr Ser
450 455 460

Trp Gln Arg Glu Ile Gln Thr Trp Ala Pro Gln Met Asn Ala Val Val
465 470 475 480

Tyr Leu Gly Asp Ile Thr Ser Arg Asn Met Ile Arg Thr His Glu Trp
485 490 495

Met His Pro Gln Thr Lys Arg Leu Lys Phe Asn Ile Leu Leu Thr Thr
500 505 510

Tyr Glu Ile Leu Leu Lys Asp Lys Ser Phe Leu Gly Gly Leu Asn Trp
515 520 525

Ala Phe Ile Gly Val Asp Glu Ala His Arg Leu Lys Asn Asp Asp Ser
530 535 540

Leu Leu Tyr Arg Thr Leu Ile Asp Phe Lys Ser Asn His Arg Leu Leu
545 550 555 560

Ile Thr Gly Thr Pro Leu Gln Asn Ser Leu Lys Glu Leu Trp Ser Leu
565 570 575

Leu His Phe Ile Met Pro Glu Lys Phe Ser Ser Trp Glu Asp Phe Glu
580 585 590

Glu Glu His Gly Lys Gly Arg Glu Tyr Gly Tyr Ala Ser Leu His Lys
595 600 605

Glu Leu Glu Pro Phe Leu Leu Arg Arg Val Lys Lys Asp Val Glu Lys

610 615 620
Ser Leu Pro Ala Lys Val Glu Gln Ile Leu Arg Met Glu Met Ser Ala
625 630 635 640
Leu Gln Lys Gln Tyr Tyr Lys Trp Ile Leu Thr Arg Asn Tyr Lys Ala
645 650 655
Leu Ser Lys Gly Ser Lys Gly Ser Thr Ser Gly Phe Leu Asn Ile Met
660 665 670
Met Glu Leu Lys Lys Cys Cys Asn His Cys Tyr Leu Ile Lys Pro Pro
675 680 685
Asp Asp Asn Glu Phe Tyr Asn Lys Gln Glu Ala Leu Gln His Leu Ile
690 695 700
Arg Ser Ser Gly Lys Leu Ile Leu Leu Asp Lys Leu Leu Ile Arg Leu
705 710 715 720
Arg Glu Arg Gly Asn Arg Val Leu Ile Phe Ser Gln Met Val Arg Met
725 730 735
Leu Asp Ile Leu Ala Glu Tyr Leu Lys Tyr Arg Gln Phe Pro Phe Gln
740 745 750
Arg Leu Asp Gly Ser Ile Lys Gly Glu Leu Arg Lys Gln Ala Leu Asp
755 760 765
His Phe Asn Ala Glu Gly Ser Glu Asp Phe Cys Phe Leu Leu Ser Thr
770 775 780
Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala Ser Ala Asp Thr Val Val
785 790 795 800
Ile Phe Asp Ser Asp Trp Asn Pro Gln Asn Asp Leu Gln Ala Gln Ala
805 810 815

Arg Ala His Arg Ile Gly Gln Lys Lys Gln Val Asn Ile Tyr Arg Leu
820 825 830
Val Thr Lys Gly Ser Val Glu Glu Asp Ile Leu Glu Arg Ala Lys Lys
835 840 845
Lys Met Val Leu Asp His Leu Val Ile Gln Arg Met Asp Thr Thr Gly
850 855 860
Lys Thr Val Leu His Thr Gly Ser Thr Pro Ser Ser Ser Thr Pro Phe
865 870 875 880
Asn Lys Glu Glu Leu Ser Ala Ile Leu Lys Phe Gly Ala Glu Glu Leu
885 890 895
Phe Lys Glu Pro Glu Gly Glu Glu Gln Glu Pro Gln Glu Met Asp Ile
900 905 910
Asp Glu Ile Leu Lys Arg Ala Glu Thr Arg Glu Asn Glu Pro Gly Pro
915 920 925
Leu Thr Val Gly Asp Glu Leu Leu Ser Gln Phe Lys Val Ala Asn Phe
930 935 940
Ser Asn Met Asp Glu Asp Asp Ile Glu Leu Glu Pro Glu Arg Asn Ser
945 950 955 960
Arg Asn Trp Glu Glu Ile Ile Pro Glu Ser Gln Arg Arg Arg Ile Glu
965 970 975
Glu Glu Arg Gln Lys Glu Leu Glu Glu Ile Tyr Met Leu Pro Arg
980 985 990
Met Arg Asn Cys Ala Lys Gln Ile Ser Phe Asn Gly Ser Glu Gly Arg
995 1000 1005
Arg Ser Arg Ser Arg Arg Tyr Ser Gly Ser Asp Ser Asp Ser Ile Thr

1010 1015 1020
Glu Arg Lys Arg Pro Lys Lys Arg Gly Arg Pro Arg Thr Ile Pro Arg
1025 1030 1035 1040
Glu Asn Ile Lys Gly Phe Ser Asp Ala Glu Ile Arg Arg Phe Ile Lys
1045 1050 1055
Ser Tyr Lys Lys Phe Gly Gly Pro Leu Glu Arg Leu Asp Ala Val Ala
1060 1065 1070
Arg Asp Ala Glu Leu Val Asp Lys Ser Glu Thr Asp Leu Arg Arg Leu
1075 1080 1085
Gly Glu Leu Val His Asn Gly Cys Ile Lys Ala Leu Lys Asp Asn Ser
1090 1095 1100
Ser Gly Gln Glu Arg Ala Gly Gly Arg Leu Gly Lys Val Lys Gly Pro
1105 1110 1115 1120
Thr Phe Arg Ile Ser Gly Val Gln Val Asn Ala Lys Leu Val Ile Ser
1125 1130 1135
His Glu Glu Glu Leu Ala Pro Leu His Lys Ser Ile Pro Ser Asp Pro
1140 1145 1150
Glu Glu Arg Lys Arg Tyr Val Ile Pro Cys His Thr Lys Ala Ala His
1155 1160 1165
Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn Leu Leu Val Gly
1170 1175 1180
Ile Tyr Glu Tyr Gly Tyr Gly Ser Trp Glu Met Ile Lys Met Asp Pro
1185 1190 1195 1200
Asp Leu Ser Leu Thr Gln Lys Ile Leu Pro Asp Asp Pro Asp Lys Lys
1205 1210 1215

Pro Gln Ala Lys Gln Leu Gln Thr Arg Ala Asp Tyr Leu Ile Lys Leu
1220 1225 1230
Leu Asn Lys Asp Leu Ala Arg Lys Glu Ala Gln Arg Leu Ala Gly Ala
1235 1240 1245
Gly Asn Ser Lys Arg Arg Lys Thr Arg Asn Lys Lys Asn Lys Met Lys
1250 1255 1260
Ala Ser Lys Ile Lys Glu Glu Ile Lys Ser Asp Ser Ser Pro Gln Pro
1265 1270 1275 1280
Ser Glu Lys Ser Asp Glu Asp Asp Glu Glu Asp Asn Lys Val Asn
1285 1290 1295
Glu Met Lys Ser Glu Asn Lys Glu Lys Ser Lys Lys Ile Pro Leu Leu
1300 1305 1310
Asp Thr Pro Val His Ile Thr Ala Thr Ser Glu Pro Val Pro Ile Ser
1315 1320 1325
Glu Glu Ser Glu Glu Leu His Gln Lys Thr Phe Ser Val Cys Lys Glu
1330 1335 1340
Arg Met Arg Pro Val Lys Ala Ala Leu Lys Gln Leu Asp Arg Pro Glu
1345 1350 1355 1360
Lys Gly Leu Ser Glu Arg Glu Gln Leu Glu His Thr Arg Gln Cys Leu
1365 1370 1375
Ile Lys Ile Gly Asp His Ile Thr Glu Cys Leu Lys Glu Tyr Thr Asn
1380 1385 1390
Pro Glu Gln Ile Lys Gln Trp Arg Lys Asn Leu Trp Ile Phe Val Ser
1395 1400 1405
Lys Phe Thr Glu Phe Asp Ala Arg Lys Leu His Lys Leu Tyr Lys His

1410

1415

1420

Ala Ile Lys Lys Arg Gln Glu Ser Gln Gln

1425

1430

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1467 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..1467

(D) OTHER INFORMATION:/note= "The sequence beginning at 1 corresponds to 2654 and that ending at 1467 corresponds to 4120"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Met Ala Ala Lys Asp Ile Ser Thr Glu Val Leu Gln Asn Pro Glu Leu

1

5

10

15

Tyr Gly Leu Arg Arg Ser His Arg Ala Ala Ala His Gln Gln Asn Tyr

20

25

30

Phe Asn Asp Ser Asp Asp Glu Asp Asp Glu Asn Ile Lys Gln Ser

35

40

45

Arg Arg Lys Arg Met Thr Thr Ile Glu Asp Asp Glu Asp Glu Phe Glu

50	55	60
Asp Glu Glu Gly Glu Glu Asp Ser Gly Glu Asp Glu Asp Glu Asp		
65	70	75
Phe Glu Glu Asp Asp Asp Tyr Tyr Gly Ser Pro Ile Lys Gln Asn Arg		
85	90	95
Ser Lys Pro Lys Ser Arg Thr Lys Ser Lys Ser Lys Pro Lys		
100	105	110
Ser Gln Ser Glu Lys Gln Ser Thr Val Lys Ile Pro Thr Arg Phe Ser		
115	120	125
Asn Arg Gln Asn Lys Thr Val Asn Tyr Asn Ile Asp Tyr Ser Asp Asp		
130	135	140
Asp Leu Leu Glu Ser Glu Asp Asp Tyr Gly Ser Glu Glu Ala Leu Ser		
145	150	155
Glu Glu Asn Val His Glu Ala Ser Ala Asn Pro Gln Pro Glu Asp Phe		
165	170	175
His Gly Ile Asp Ile Val Ile Asn His Arg Leu Lys Thr Ser Leu Glu		
180	185	190
Glu Gly Lys Val Leu Glu Lys Thr Val Pro Asp Leu Asn Asn Cys Lys		
195	200	205
Glu Asn Tyr Glu Phe Leu Ile Lys Trp Thr Asp Glu Ser His Leu His		
210	215	220
Asn Thr Trp Glu Thr Tyr Glu Ser Ile Gly Gln Val Arg Gly Leu Lys		
225	230	235
Arg Leu Asp Asn Tyr Cys Lys Gln Phe Ile Ile Glu Asp Gln Gln Val		
245	250	255

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Arg Leu Asp Pro Tyr Val Thr Ala Glu Asp Ile Glu Ile Met Asp Met
260 265 270
Glu Arg Glu Arg Arg Leu Asp Glu Phe Glu Glu Phe His Val Pro Glu
275 280 285
Arg Ile Ile Asp Ser Gln Arg Ala Ser Leu Glu Asp Gly Thr Ser Gln
290 295 300
Leu Gln Tyr Leu Val Lys Trp Arg Arg Leu Asn Tyr Asp Glu Ala Thr
305 310 315 320
Trp Glu Asn Ala Thr Asp Ile Val Lys Leu Ala Pro Glu Gln Val Lys
325 330 335
His Phe Gln Asn Arg Glu Asn Ser Lys Ile Leu Pro Gln Tyr Ser Ser
340 345 350
Asn Tyr Thr Ser Gln Arg Pro Arg Phe Glu Lys Leu Ser Val Gln Pro
355 360 365
Pro Phe Ile Lys Gly Gly Glu Leu Arg Asp Phe Gln Leu Thr Gly Ile
370 375 380
Asn Trp Met Ala Phe Leu Trp Ser Lys Gly Asp Asn Gly Ile Leu Ala
385 390 395 400
Asp Glu Met Gly Leu Gly Lys Thr Val Gln Thr Val Ala Phe Ile Ser
405 410 415
Trp Leu Ile Phe Ala Arg Arg Gln Asn Gly Pro His Ile Ile Val Val
420 425 430
Pro Leu Ser Thr Met Pro Ala Trp Leu Asp Thr Phe Glu Lys Trp Ala
435 440 445
Pro Asp Leu Asn Cys Ile Cys Tyr Met Gly Asn Gln Lys Ser Arg Asp

450 455 460
Thr Ile Arg Glu Tyr Glu Phe Tyr Thr Asn Pro Arg Ala Lys Gly Lys
465 470 475 480
Lys Thr Met Lys Phe Asn Val Leu Leu Thr Thr Tyr Glu Tyr Ile Leu
485 490 495
Lys Asp Arg Ala Glu Leu Gly Ser Ile Lys Trp Gln Phe Met Ala Val
500 505 510
Asp Glu Ala His Arg Leu Lys Asn Ala Glu Ser Ser Leu Tyr Glu Ser
515 520 525
Leu Asn Ser Phe Lys Val Ala Asn Arg Met Leu Ile Thr Gly Thr Pro
530 535 540
Leu Gln Asn Asn Ile Lys Glu Leu Ala Ala Leu Val Asn Phe Leu Met
545 550 555 560
Pro Gly Arg Phe Thr Ile Asp Gln Glu Ile Asp Phe Glu Asn Gln Asp
565 570 575
Glu Glu Gln Glu Glu Tyr Ile His Asp Leu His Arg Arg Ile Gln Pro
580 585 590
Phe Ile Leu Arg Arg Leu Lys Lys Asp Val Glu Lys Ser Leu Pro Ser
595 600 605
Lys Thr Glu Arg Ile Leu Arg Val Glu Leu Ser Asp Val Gln Thr Glu
610 615 620
Tyr Tyr Lys Asn Ile Leu Thr Lys Asn Tyr Ser Ala Leu Thr Ala Gly
625 630 635 640
Ala Lys Gly Gly His Phe Ser Leu Leu Asn Ile Met Asn Glu Leu Lys
645 650 655

Lys Ala Ser Asn His Pro Tyr Leu Phe Asp Asn Ala Glu Glu Arg Val
660 665 670
Leu Gln Lys Phe Gly Asp Gly Lys Met Thr Arg Glu Asn Val Leu Arg
675 680 685
Gly Leu Ile Met Ser Ser Gly Lys Met Val Leu Leu Asp Gln Leu Leu
690 695 700
Thr Arg Leu Lys Asp Gly His Arg Val Leu Ile Phe Ser Gln Met
705 710 715 720
Val Arg Met Leu Asp Ile Leu Gly Asp Tyr Leu Ser Ile Lys Gly Ile
725 730 735
Asn Phe Gln Arg Leu Asp Gly Thr Val Pro Ser Ala Gln Arg Arg Ile
740 745 750
Ser Ile Asp His Phe Asn Ser Pro Asp Ser Asn Asp Phe Val Phe Leu
755 760 765
Leu Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Met Thr Ala Asp
770 775 780
Thr Val Val Ile Phe Asp Ser Asp Trp Asn Pro Gln Ala Asp Leu Gln
785 790 795 800
Ala Met Ala Arg Ala His Arg Ile Gly Gln Lys Asn His Val Met Val
805 810 815
Tyr Arg Leu Val Ser Lys Asp Thr Val Glu Glu Val Leu Glu Arg
820 825 830
Ala Arg Lys Lys Met Ile Leu Glu Tyr Ala Ile Ile Ser Leu Gly Val
835 840 845
Thr Asp Gly Asn Lys Tyr Thr Lys Lys Asn Glu Pro Asn Ala Gly Glu

850

855

860

Leu Ser Ala Ile Leu Lys Phe Gly Ala Gly Asn Met Phe Thr Ala Thr

865

870

875

880

Asp Asn Gln Lys Lys Leu Glu Asp Leu Asn Leu Asp Asp Val Leu Asn

885

890

895

His Ala Glu Asp His Val Thr Thr Pro Asp Leu Gly Glu Ser His Leu

900

905

910

Gly Gly Glu Glu Phe Leu Lys Gln Phe Glu Val Thr Asp Tyr Lys Ala

915

920

925

Asp Ile Asp Trp Asp Asp Ile Ile Pro Glu Glu Leu Lys Lys Leu

930

935

940

Gln Asp Glu Glu Gln Lys Arg Lys Asp Glu Glu Tyr Val Lys Glu Gln

945

950

955

960

Leu Glu Met Met Asn Arg Arg Asp Asn Ala Leu Lys Lys Ile Lys Asn

965

970

975

Ser Val Asn Gly Asp Gly Thr Ala Ala Asn Ser Asp Ser Asp Asp Asp

980

985

990

Ser Thr Ser Arg Ser Ser Arg Arg Ala Arg Ala Asn Asp Met Asp

995

1000

1005

Ser Ile Gly Glu Ser Glu Val Arg Ala Leu Tyr Lys Ala Ile Leu Lys

1010

1015

1020

Phe Gly Asn Leu Lys Glu Ile Leu Asp Glu Leu Ile Ala Asp Gly Thr

1025

1030

1035

1040

Leu Pro Val Lys Ser Phe Glu Lys Tyr Gly Glu Thr Tyr Asp Glu Met

1045

1050

1055

Met Glu Ala Ala Lys Asp Cys Val His Glu Glu Glu Lys Asn Arg Lys
1060 1065 1070
Glu Ile Leu Glu Lys Leu Glu Lys His Ala Thr Ala Tyr Arg Ala Lys
1075 1080 1085
Leu Lys Ser Gly Glu Ile Lys Ala Glu Asn Gln Pro Lys Asp Asn Pro
1090 1095 1100
Leu Thr Arg Leu Ser Leu Lys Lys Arg Glu Lys Lys Ala Val Leu Phe
1105 1110 1115 1120
Asn Phe Lys Gly Val Lys Ser Leu Asn Ala Glu Ser Leu Leu Ser Arg
1125 1130 1135
Val Glu Asp Leu Lys Tyr Leu Lys Asn Leu Ile Asn Ser Asn Tyr Lys
1140 1145 1150
Asp Asp Pro Leu Lys Phe Ser Leu Gly Asn Asn Thr Pro Lys Pro Val
1155 1160 1165
Gln Asn Trp Ser Ser Asn Trp Thr Lys Glu Glu Asp Glu Lys Leu Leu
1170 1175 1180
Ile Gly Val Phe Lys Tyr Gly Tyr Gly Ser Trp Thr Gln Ile Arg Asp
1185 1190 1195 1200
Asp Pro Phe Leu Gly Ile Thr Asp Lys Ile Phe Leu Asn Glu Val His
1205 1210 1215
Asn Pro Val Ala Lys Lys Ser Ala Ser Ser Ser Asp Thr Thr Pro Thr
1220 1225 1230
Pro Ser Lys Lys Gly Lys Gly Ile Thr Gly Ser Ser Lys Lys Val Pro
1235 1240 1245
Gly Ala Ile His Leu Gly Arg Arg Val Asp Tyr Leu Leu Ser Phe Leu

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1250 1255 1260
Arg Gly Gly Leu Asn Thr Lys Ser Pro Ser Ala Asp Ile Gly Ser Lys
1265 1270 1275 1280
Lys Leu Pro Thr Gly Pro Ser Lys Lys Arg Gln Arg Lys Pro Ala Asn
1285 1290 1295
His Ser Lys Ser Met Thr Pro Glu Ile Thr Ser Ser Glu Pro Ala Asn
1300 1305 1310
Gly Pro Pro Ser Lys Arg Met Lys Ala Leu Pro Lys Gly Pro Ala Ala
1315 1320 1325
Leu Ile Asn Asn Thr Arg Leu Ser Pro Asn Ser Pro Thr Pro Pro Leu
1330 1335 1340
Lys Ser Lys Val Ser Arg Asp Asn Gly Thr Arg Gln Ser Ser Asn Pro
1345 1350 1355 1360
Ser Ser Gly Ser Ala His Glu Lys Glu Tyr Asp Ser Met Asp Glu Glu
1365 1370 1375
Asp Cys Arg His Thr Met Ser Ala Ile Arg Thr Ser Leu Lys Arg Leu
1380 1385 1390
Arg Arg Gly Gly Lys Ser Leu Asp Arg Lys Glu Trp Ala Lys Ile Leu
1395 1400 1405
Lys Thr Glu Leu Thr Thr Ile Gly Asn His Ile Glu Ser Gln Lys Gly
1410 1415 1420
Ser Ser Arg Lys Ala Ser Pro Glu Lys Tyr Arg Lys His Leu Trp Ser
1425 1430 1435 1440
Tyr Ser Ala Asn Phe Trp Pro Ala Asp Val Lys Ser Thr Lys Leu Met
1445 1450 1455

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Ala Met Tyr Asp Lys Ile Thr Glu Ser Gln Lys

1460

1465

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Ala Val Glu Ala Asp Gly Asp Pro Asn Ala Gly Phe Glu Lys Ser Lys

1

5

10

15

Glu Leu Gly Glu Ile Gln Tyr Leu Ile Lys Trp Lys Gly Trp Ser His

20

25

30

Ile His Asn Thr Trp Glu Thr Glu Glu Thr Leu Lys Gln Gln Asn Val

35

40

45

Lys Gly Met Asn Lys Leu Asp Asn Tyr Lys Lys

50

55

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Ala Val Glu Ala Asp Gly Asp Pro Asn Ala Gly Phe Glu Arg Asn Lys

1 5 10 15

Glu Pro Gly Asp Ile Gln Tyr Leu Ile Lys Trp Lys Gly Trp Ser His

20 25 30

Ile His Asn Thr Trp Glu Thr Glu Glu Thr Leu Lys Gln Gln Asn Val

35 40 45

Arg Gly Asn Lys Lys Leu Asp Asn Tyr Lys Lys

50 55

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Glu Gly Lys Val Leu Glu Lys Thr Val Pro Asp Leu Asn Asn Cys Lys

1 5 10 15

Glu Asn Tyr Glu Phe Leu Ile Lys Trp Thr Asp Glu Ser His Leu His

20 25 30

Asn Thr Trp Glu Thr Tyr Glu Ser Ile Gly Gln Val Arg Gly Leu Lys

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35

40

45

Arg Leu Asp Asn Tyr Cys Lys

50

55

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Glu Glu Glu Glu Glu Tyr Ala Val Glu Lys Ile Ile Asp Arg Arg Val

1 5 10 15

Arg Lys Gly Lys Val Glu Tyr Tyr Leu Lys Trp Lys Gly Tyr Pro Glu

20 25 30

Thr Glu Asn Thr Trp Glu Pro Glu Asn Asn Leu Asp Cys Gln Asp Leu

35 40 45

Ile Gln Gln Tyr

50

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Glu Asp Glu Glu Glu Tyr Val Val Glu Lys Val Leu Asp Arg Arg Val

1

5

10

15

Val Lys Gly Lys Gln Val Glu Tyr Leu Leu Lys Trp Lys Gly Phe Ser

20

25

30

Glu Glu His Asn Thr Trp Glu Pro Glu Lys Asn Leu Asp Cys Pro Glu

35

40

45

Leu Ile Ser Glu Phe

50

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Glu Glu Glu Glu Glu Tyr Val Val Glu Lys Val Leu Asp Arg Arg Val

1

5

10

15

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Val Lys Gly Lys Val Glu Tyr Leu Leu Lys Trp Lys Gly Phe Ser Asp
20 25 30
Glu Asp Asn Thr Trp Glu Pro Glu Glu Asn Leu Asp Cys Pro Asp Leu
35 40 45
Ile Ala Glu Phe
50

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Ala Glu Pro Glu Glu Phe Val Val Glu Lys Val Leu Asp Arg Arg Val
1 5 10 15
Val Asn Gly Lys Val Glu Tyr Phe Leu Lys Trp Lys Gly Phe Thr Asp
20 25 30
Ala Asp Asn Thr Trp Glu Pro Glu Asn Leu Asp Cys Pro Glu Leu
35 40 45
Ile Glu Asp Phe
50

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(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Pro Val Asp Leu Val Tyr Ala Ala Glu Lys Ile Ile Gln Lys Arg Val
1 5 10 15

Lys Lys Gly Val Val Glu Tyr Arg Val Lys Trp Lys Gly Trp Asn Gln
20 25 30

Arg Tyr Asn Thr Trp Glu Pro Glu Asn Asn Ile Leu Asp Arg Arg Leu
35 40 45

Ile Asp Ile Tyr
50

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Val Gly Glu Gln Val Phe Ala Ala Glu Cys Ile Leu Ser Lys Arg Leu
1 5 10 15
Arg Lys Gly Lys Leu Glu Tyr Leu Val Lys Trp Arg Gly Trp Ser Ser
20 25 30
Lys His Asn Ser Trp Glu Pro Glu Glu Asn Ile Leu Asp Pro Arg Leu
35 40 45
Leu Leu Ala Phe
50

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AGATATTCTG GATCTGATAG TGATTCAATC TCGGAAAGGA AACGGCCGAA GAAACGTGGG 60
CGACCCCCGCA CTATCCCTCG GGAGAAATATT AAAGGATTAA GTGATGCGGA G 111

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

AGATATTCTG GATCTGATAG TGACTCCATC ACAGAAAGAA AACGGCCAAA AAAGCGTGGA 60

AGACCTCGAA CCATTCCTCG AGAAAATATT AAAGGATTAA GTGATGCAGA G 111

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CTCCATCTCG GAAAGGAAAC GGCAAAAAAA GCGTGGAAAGA CCACGAACTA TTCCTCGAGA 60

AAATATA 67

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

AGATATTCTG GATCTGATAG TGATTCCATC TCAGAAAGAA AACGACCAAA AAAACGTGGA 60
CGACCACGAA CTATTCCCCG TGAAAACATT AAAGGATTAA GTGATGCAGA G 111

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CTCCATCTCA GAAAGAAAAC GACCAAGAAA ACGTGGACGA CCACGAACTA TTCCCTCGTGA 60
AAATATT 67

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GATCTGATAG TGACTCCATC TCAGAAAGAA AACGACCAAG AAAACGTGGA CGACCACGAA 60
CTATCCCTCG GGAGAATATT AAAGGATTAA GCGATGCAGA GATTAGGCGG T 111

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

ATATTCTGGA TCTGATAGTG AYTC

24

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

AGATATTCCG GATCTGATAG TGA

23

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- 116 -

- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- (A) DESCRIPTION: /desc = "Synthetic DNA Primer"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

TTTCCTAAAT CGCTACGTCT

20